

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/582,973  
Source: IFWP  
Date Processed by STIC: 6/26/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

AMC – STIC Systems Branch – 03/02/06

| <u>ERROR DETECTED</u>   | <u>SUGGESTED CORRECTION</u>  | SERIAL NUMBER: <u>10/582,973</u> |
|---|--|----------------------------------|
| <b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b> |  |                                  |
| 1 <u>      </u> Wrapped Nucleics<br>Wrapped Aminos  | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor <b>after</b> creating it. Please adjust your right margin to .3; this will prevent "wrapping."  |                                  |
| 2 <u>      </u> Invalid Line Length   | The rules require that a line <b>not exceed</b> 72 characters in length. This includes white spaces.   |                                  |
| 3 <u>      </u> Misaligned Amino<br>Numbering   | The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do <b>not</b> use tab codes between numbers; use <b>space characters</b> , instead.   |                                  |
| 4 <u>      </u> Non-ASCII   | The submitted file was <b>not</b> saved in ASCII(DOS) text, as <b>required</b> by the Sequence Rules. <b>Please ensure your subsequent submission is saved in ASCII text.</b>  |                                  |
| 5 <u>      </u> Variable Length   | Sequence(s) <u>      </u> contain n's or Xaa's representing more than one residue. <b>Per Sequence Rules, each n or Xaa can only represent a single residue.</b> Please present the <b>maximum</b> number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.   |                                  |
| 6 <u>      </u> PatentIn 2.0<br>"bug"   | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <u>      </u> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. <b>This applies to the mandatory &lt;220&gt;-&lt;223&gt; sections for Artificial or Unknown sequences.</b>  |                                  |
| 7 <u>      </u> Skipped Sequences<br>(OLD RULES)  | Sequence(s) <u>      </u> missing. If intentional, please insert the following lines for <b>each</b> skipped sequence:<br>(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)<br>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)<br>This sequence is intentionally skipped<br>Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to <b>include</b> the skipped sequences. |                                  |
| 8 <u>      </u> Skipped Sequences<br>(NEW RULES)  | Sequence(s) <u>      </u> missing. If <b>intentional</b> , please insert the following lines for <b>each</b> skipped sequence.<br><210> sequence id number<br><400> sequence id number<br>000  |                                  |
| 9 <u>      </u> Use of n's or Xaa's<br>(NEW RULES)  | Use of n's and/or Xaa's have been detected in the Sequence Listing.<br>Per 1.823 of Sequence Rules, use of <220>-<223> is <b>MANDATORY</b> if n's or Xaa's are present.<br>In <220> to <223> section, please explain location of <b>n</b> or <b>Xaa</b> , and which residue <b>n</b> or <b>Xaa</b> represents.   |                                  |
| 10 <u>      </u> Invalid <213><br>Response  | Per 1.823 of Sequence Rules, the only <b>valid</b> <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is <b>required</b> when <213> response is Unknown or is Artificial Sequence. (see item 11 below)   |                                  |
| 11 <u>      </u> Use of <220>   | Sequence(s) <u>      </u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is <b>MANDATORY</b> if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules  |                                  |
| 12 <u>      </u> PatentIn 2.0<br>"bug"  | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.  |                                  |
| 13 <u>      </u> Misuse of n/Xaa  | <b>"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid</b>  |                                  |



IFWP

## RAW SEQUENCE LISTING

DATE: 06/26/2006

PATENT APPLICATION: US/10/582,973

TIME: 13:30:45

Input Set : A:\sequence list.txt

Output Set: N:\CRF4\06262006\J582973.raw

2 <110> APPLICANT: Toshikazu Nakamura  
W--> 3 <120> TITLE OF INVENTION: Glycosylation-deficient hepatocyte growth factor  
W--> 4 <130> FILE REFERENCE: N13F1456  
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/582,973  
C--> 5 <141> CURRENT FILING DATE: 2006-06-15  
W--> 5 <160> NUMBER OF SEQ ID: 8

## ERRORED SEQUENCES

106 <210> SEQ ID NO: 2  
107 <211> LENGTH: 723  
108 <212> TYPE: PRT  
109 <213> ORGANISM: Homo sapiens  
W--> 110 <220> FEATURE: Hepatocyte growth factor of five amino acids-deleted type  
111 <223> OTHER INFORMATION: move this to 2237 line. 2207  
W--> 112 <400> SEQUENCE: 2

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 113 | Met | Trp | Val | Thr | Lys | Leu | Leu | Pro | Ala | Leu | Leu | Gln | His | Val | Leu |
| 114 |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| 115 | Leu | His | Leu | Leu | Leu | Leu | Pro | Ile | Ala | Ile | Pro | Tyr | Ala | Glu | Gly |
| 116 |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |
| 117 | Arg | Lys | Arg | Arg | Asn | Thr | Ile | His | Glu | Phe | Lys | Lys | Ser | Ala | Lys |
| 118 |     |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |
| 119 | Thr | Leu | Ile | Lys | Ile | Asp | Pro | Ala | Leu | Lys | Ile | Lys | Thr | Lys | Val |
| 120 |     |     |     |     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |
| 121 | Asn | Thr | Ala | Asp | Gln | Cys | Ala | Asn | Arg | Cys | Thr | Arg | Asn | Lys | Gly |
| 122 | 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     | 80  |     |
| 123 | Pro | Phe | Thr | Cys | Lys | Ala | Phe | Val | Phe | Asp | Lys | Ala | Arg | Lys | Gln |
| 124 |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     | 95  |     |
| 125 | Leu | Trp | Phe | Pro | Phe | Asn | Ser | Met | Ser | Ser | Gly | Val | Lys | Lys | Glu |
| 126 |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     | 110 |     |
| 127 | Gly | His | Glu | Phe | Asp | Leu | Tyr | Glu | Asn | Lys | Asp | Tyr | Ile | Arg | Asn |
| 128 |     |     |     |     | 115 |     |     |     |     | 120 |     |     |     | 125 |     |
| 129 | Ile | Ile | Gly | Lys | Gly | Arg | Ser | Tyr | Lys | Gly | Thr | Val | Ser | Ile | Thr |
| 130 |     |     |     |     | 130 |     |     |     |     | 135 |     |     |     | 140 |     |
| 131 | Ser | Gly | Ile | Lys | Cys | Gln | Pro | Trp | Ser | Ser | Met | Ile | Pro | His | Glu |
| 132 | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     | 160 |     |
| 133 | Ser | Tyr | Arg | Gly | Lys | Asp | Leu | Gln | Glu | Asn | Tyr | Cys | Arg | Asn | Pro |
| 134 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     | 175 |     |
| 135 | Gly | Glu | Glu | Gly | Pro | Trp | Cys | Phe | Thr | Ser | Asn | Pro | Glu | Val | Arg |
| 136 |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     | 190 |     |
| 137 | Tyr | Glu | Val | Cys | Asp | Ile | Pro | Gln | Cys | Ser | Glu | Val | Glu | Cys | Met |
| 138 |     |     |     |     | 195 |     |     |     |     | 200 |     |     |     | 205 |     |

Does Not Comply  
Corrected Diskette Needed

never has  
a response.  
It is a  
"header" only

## RAW SEQUENCE LISTING

DATE: 06/26/2006

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TIME: 13:30:45

Input Set : A:\sequence list.txt

Output Set: N:\CRF4\06262006\J582973.raw

```

139 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly
140      210      215      220
141 Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe
142 225      230      235      240
143 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg
144      245      250      255
145 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His
146      260      265      270
147 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr Met
148      275      280      285
149 Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly Gln
150      290      295      300
151 Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile Pro
152 305      310      315      320
153 Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr Pro
154      325      330      335
155 Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn Pro
156      340      345      350
157 Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile Arg
158      355      360      365
159 Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly Gln
160      370      375      380
161 Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser Gln
162 385      390      395      400
163 Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu Asp5
164      405      410      415
165 Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn Glu
166      420      425      430
167 Asn Tyr Cys Arg Asn Pro Asp Asp Ala His Gly Pro Trp Cys Tyr
168      435      440      445
169 Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg Cys
170      450      455      460
171 Glu Gly Asp Thr Thr Pro Thr Ile Val Asn Leu Asp His Pro Val Ile
172 465      470      475      480
173 Ser Cys Ala Lys Thr Lys Gln Leu Arg Val Val Asn Gly Ile Pro Thr
174      485      490      495
175 Arg Thr Asn Ile Gly Trp Met Val Ser Leu Arg Tyr Arg Asn Lys His
176      500      505      510
177 Ile Cys Gly Gly Ser Leu Ile Lys Glu Ser Trp Val Leu Thr Ala Arg
178      515      520      525
179 Gln Cys Phe Pro Ser Arg Asp Leu Lys Asp Tyr Glu Ala Trp Leu Gly
180      530      535      540
181 Ile His Asp Val His Gly Arg Gly Asp Glu Lys Cys Lys Gln Val Leu
182 545      550      555      560
183 Asn Val Ser Gln Leu Val Tyr Gly Pro Glu Gly Ser Asp Leu Val Leu
184      565      570      575
185 Met Lys Leu Ala Arg Pro Ala Val Leu Asp Asp Phe Val Ser Thr Ile
186      580      585      590
187 Asp Leu Pro Asn Tyr Gly Cys Thr Ile Pro Glu Lys Thr Ser Cys Ser

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/582,973

DATE: 06/26/2006  
TIME: 13:30:45

Input Set : A:\sequence list.txt  
Output Set: N:\CRF4\06262006\J582973.raw

188            595                            600                            605  
189 Val Tyr Gly Trp Gly Tyr Thr Gly Leu Ile Asn Tyr Asp Gly Leu Leu  
190            610                            615                            620  
191 Arg Val Ala His Leu Tyr Ile Met Gly Asn Glu Lys Cys Ser Gln His  
192 625                            630                            635                            640  
193 His Arg Gly Lys Val Thr Leu Asn Glu Ser Glu Ile Cys Ala Gly Ala  
194                            645                            650                            655  
195 Glu Lys Ile Gly Ser Gly Pro Cys Glu Gly Asp Tyr Gly Gly Pro Leu  
196                            660                            665                            670  
197 Val Cys Glu Gln His Lys Met Arg Met Val Leu Gly Val Ile Val Pro5  
198            675                            680                            685  
199 Gly Arg Gly Cys Ala Ile Pro Asn Arg Pro Gly Ile Phe Val Arg Val  
200            690                            695                            700  
201 Ala Tyr Tyr Ala Lys Trp Ile His Lys Ile Ile Leu Thr Tyr Lys Val  
202 705                            710                            715                            720  
E--> 203 Pro Gln Ser  
250 <210> SEQ ID NO: 4  
251 <211> LENGTH: 39  
252 <212> TYPE: DNA  
253 <213> ORGANISM: Artificial Sequence  
W--> 254 ~~(220) FEATURE:~~ *insert <2207*  
254 <223> OTHER INFORMATION: *explain Artificial Sequence wherever <2217, <2227, or <2237 is shown 39*  
EOK 255 <400> SEQUENCE: 4  
256 tgcgctgaca atactatgca agacactgat gttcctttg  
258 <210> SEQ ID NO: 5  
259 <211> LENGTH: 41  
260 <212> TYPE: DNA  
261 <213> ORGANISM: Artificial Sequence  
W--> 262 ~~(220) FEATURE:~~ *insert <2207*  
262 <223> OTHER INFORMATION: *explain (see item 11)*  
EOK 263 <400> SEQUENCE: 5  
264 ggcaaaaatt atatggggcca gttatcccaa acaagatctg g  
266 <210> SEQ ID NO: 6  
267 <211> LENGTH: 38  
268 <212> TYPE: DNA  
269 <213> ORGANISM: Artificial Sequence  
W--> 270 ~~(220) FEATURE:~~ *insert <2207*  
270 <223> OTHER INFORMATION: *see item 11*  
EOK 271 <400> SEQUENCE: 6  
272 tgcaaacagg ttctccaagt ttcccagctg gtatatgg  
274 <210> SEQ ID NO: 7  
275 <211> LENGTH: 38  
276 <212> TYPE: DNA  
277 <213> ORGANISM: Artificial Sequence  
W--> 278 ~~(220) FEATURE:~~ *insert <2207*  
278 <223> OTHER INFORMATION: *(see item 11)*  
EOK 279 <400> SEQUENCE: 7  
280 gggaagggtga ctctgcaaga gtctgaaata tgtgtctgg  
282 <210> SEQ ID NO: 8

*723 delete - number the amino acids under every 5 amino acids*

*(see item 11 on Error Summary sheet)*

*41*

*38*

*38*

## RAW SEQUENCE LISTING

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TIME: 13:30:45

Input Set : A:\sequence list.txt

Output Set: N:\CRF4\06262006\J582973.raw

283 &lt;211&gt; LENGTH: 38

284 &lt;212&gt; TYPE: DNA

285 &lt;213&gt; ORGANISM: Artificial Sequence

W--> 286 ~~<220> FEATURE:~~ *7 insert 2207*

286 &lt;223&gt; OTHER INFORMATION:

OK-> 287 <400> SEQUENCE: 8 *see item 11*

288 .ggtgatacca cacctggaat agtcaattta gaccatcc

38

10/582,973

5

<210> 1

<211> 728

<212> PRT

<213> Homo sapiens

<220> Hepatocyte growth factor

<223> 1

<400> 1

move to <223> line

10/582,973 6

<210> 3

<211> 2172 *sapiens*

<212> DNA

<213> Homo sapiens

*move to <223> here*

<220> Hepatocyte growth factor of five amino acids-deleted type

<223> 3

<400> 3



VERIFICATION SUMMARY

DATE: 06/26/2006

PATENT APPLICATION: US/10/582,973

TIME: 13:30:46

Input Set : A:\sequence list.txt

Output Set: N:\CRF4\06262006\J582973.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier  
L:4 M:283 W: Missing Blank Line separator, <130> field identifier  
L:5 M:270 C: Current Application Number differs, Replaced Current Application No  
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:5 M:283 W: Missing Blank Line separator, <160> field identifier  
L:6 M:283 W: Missing Blank Line separator, <210> field identifier  
L:10 M:283 W: Missing Blank Line separator, <220> field identifier  
L:10 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:12 M:283 W: Missing Blank Line separator, <400> field identifier  
L:12 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:11  
L:110 M:283 W: Missing Blank Line separator, <220> field identifier  
L:110 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:112 M:283 W: Missing Blank Line separator, <400> field identifier  
L:112 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:111  
L:203 M:252 E: No. of Seq. differs, <211> LENGTH:Input:723 Found:688 SEQ:2  
L:209 M:283 W: Missing Blank Line separator, <220> field identifier  
L:209 M:256 W: Invalid Numeric Header Field, <220> has non-blank data  
L:211 M:283 W: Missing Blank Line separator, <400> field identifier  
L:211 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:210  
L:254 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4  
L:255 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4  
L:255 M:283 W: Missing Blank Line separator, <400> field identifier  
L:255 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:254  
L:262 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5  
L:263 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5  
L:263 M:283 W: Missing Blank Line separator, <400> field identifier  
L:263 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:262  
L:270 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6  
L:271 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6  
L:271 M:283 W: Missing Blank Line separator, <400> field identifier  
L:271 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:270  
L:278 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7  
L:279 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:7  
L:279 M:283 W: Missing Blank Line separator, <400> field identifier  
L:279 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:278  
L:286 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:8  
L:287 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8  
L:287 M:283 W: Missing Blank Line separator, <400> field identifier  
L:287 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:286